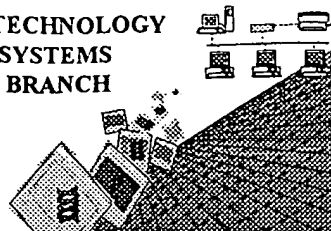


1644

#17

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/634,287B

Source:

1602

Date Processed by STIC:

12/13/2002

RECEIVED

DEC 20 2002

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

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1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/634,287B

DATE: 12/13/2002

TIME: 14:49:42

Input Set : A:\DM6909.ST25.txt

Output Set: N:\CRF4\12132002\I634287B.raw

3 <110> APPLICANT: BRISTOL-MYERS SQUIBB COMPANY
 5 <120> TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
 7 <130> FILE REFERENCE: DM6090 DIV
 9 <140> CURRENT APPLICATION NUMBER: 09/634,287B
 10 <141> CURRENT FILING DATE: 2000-08-09
 12 <150> PRIOR APPLICATION NUMBER: 60/053,850
 13 <151> PRIOR FILING DATE: 1997-07-25
 15 <150> PRIOR APPLICATION NUMBER: 60/055,836
 16 <151> PRIOR FILING DATE: 1997-08-15
 18 <150> PRIOR APPLICATION NUMBER: 60/062,169
 19 <151> PRIOR FILING DATE: 1997-10-16
 21 <160> NUMBER OF SEQ ID NOS: 48
 23 <170> SOFTWARE: PatentIn version 3.1

ERRORED SEQUENCES

1243 <210> SEQ ID NO: 48
 1244 <211> LENGTH: 16
 1245 <212> TYPE: PRT
 1246 <213> ORGANISM: dog
 1248 <400> SEQUENCE: 48
 1250 Thr Glu Pro Thr Val Ser Gln Glu Leu Ala Gln Arg Pro Pro Val Thr
 1251 1 5 10 15
 E--> 1257 1

Does Not Comply
 Corrected Diskette Needed
 pp 1-3

delete

see p. 2 for more errors

2

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/634,287B

DATE: 12/18/2002

TIME: 18:25:38

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\12182002\I634287B.raw

371 770 775 780
 374 Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg Leu Arg Tyr Ser Phe
 375 785 790 795 800
 378 Phe Val Pro Arg Pro Thr Pro Ser Thr Pro Arg Pro Thr Pro Gln Asp
 379 805 810 815
 382 Trp Leu His Arg Arg Ala Gln Ile Leu Glu Ile Leu Arg Arg Arg Pro
 383 820 825 830
 386 Trp Ala Gly Arg Lys
 387 835

390 <210> SEQ ID NO: 3
 391 <211> LENGTH: 0
 392 <212> TYPE: DNA
 393 <213> ORGANISM: Unknown
 395 <220> FEATURE:
 396 <223> OTHER INFORMATION: Blank Sequence
 398 <400> SEQUENCE: 3

W--> 399 000

401 <210> SEQ ID NO: 4
 402 <211> LENGTH: 26
 403 <212> TYPE: PRT
 404 <213> ORGANISM: Bos taurus
 406 <400> SEQUENCE: 4
 408 Phe Ala Ser Leu Ser Arg Val Glu Thr Leu Val Val Ala Asp Asp Lys
 409 1 5 10 15
 412 Met Ala Ala Phe His Gly Ala Gly Leu Lys
 413 20 25

416 <210> SEQ ID NO: 5
 417 <211> LENGTH: 7
 418 <212> TYPE: PRT
 419 <213> ORGANISM: Bos taurus
 421 <400> SEQUENCE: 5
 423 Tyr Thr Gly Val Ala Pro Arg
 424 1 5
 427 <210> SEQ ID NO: 6
 428 <211> LENGTH: 11
 429 <212> TYPE: PRT
 430 <213> ORGANISM: Bos taurus
 432 <400> SEQUENCE: 6
 434 Ala Leu Gly Tyr Tyr Tyr Val Leu Asp Pro Arg
 435 1 5 10

438 <210> SEQ ID NO: 7
 439 <211> LENGTH: 21
 440 <212> TYPE: DNA
 441 <213> ORGANISM: Mus musculus
 443 <400> SEQUENCE: 7
 444 ggggggtgggtg tccagttctc c
 447 <210> SEQ ID NO: 8
 448 <211> LENGTH: 23
 449 <212> TYPE: DNA

*delete. Please use
 format shown
 in item 8 on Error
 Summary Sheet,
 for intentionally
 skipped
 sequences.*

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/634,287B

DATE: 12/18/2002
TIME: 18:25:39

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\12182002\I634287B.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:21; Xaa Pos. 12

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/634,287B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
(OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
(NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.